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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Grotendorst, Gary R.
 Bradham Jr., Douglas M.,
- 5 (ii) TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
 - (iii) NUMBER OF SEQUENCES: 2
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Spensley Horn Jubas & Lubitz
 - (B) STREET: 4225 Executive Square, Suite 1400
 - (C) CITY: La Jolla
 - (D) STATE: CA
 - (E) COUNTRY: US
 - (F) ZIP: 92037
- 15 (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- 20 (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE: 30-AUG-1991
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
- 25 (A) NAME: Wetherell, Jr. Ph.D., John W.
 - (B) REGISTRATION NUMBER: 31.678
 - (C) REFERENCE/DOCKET NUMBER: PD-1294
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 619-455-5100
- 30 (B) TELEFAX: 619-455-5110

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(2) INFORMATION FOR SEQ ID NO:1:

5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2075 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(vii) IMMEDIATE SOURCE: (B) CLONE: DB60R32	
10	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1301177	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
	CCCGGCCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG	60
15	CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCCGCA	120
	GTGCCAACC ATG ACC GCC GCC AGT ATG GGC CCC GTC CGC GTC GCC TTC Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe 1 5 10	168
20	GTG GTC CTC GCC CTC TGC AGC CGG CCG GCC GTC GGC CAG AAC TGC Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys 20 25	216
	AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC CCG GCG Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala 30 35 40 45	264
25	GGC GTG AGC CTC GTG CTG GAC GGC TGC GGC TGC TGC CGC GTC TGC GCC Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala 50 55 60	312
30	AAG CAG CTG GGC GAG CTG TGC ACC GAG CGC GAC CCC TGC GAC CCG CAC Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His 65 70 75	360

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		CTC Leu 80									408
5		ACC Thr									456
		AGC Ser			Phe						504
10		GAC Asp				-					552
15		CCC Pro									600
		TGC Cys 160									648
20		GGG Gly									696
·		CCA Pro									744
25		GCC Ala									792
30		GAC Asp									840
•		AGG Arg 240		_	_						888



				ATC														936
5				TGC Cys														984
				GAC Asp										Thr				1032
10				TTC Phe 305														1080
15				AAG Lys														1128
				GAA Glu												GCA 1	C	1177
	GAAG	CCAC	AG A	AGTGA	GAGA	C AI	TAAC	TCAI	TAG	ACTG	GAA	CTTG	AACI	GA 1	TCAC	ATCT	3	1237
20	ATTI	TTCC	GT A	AAAA	TGAT	T TC	AGTA	GCAC	AAG	TTAT	TTA	AATC	TGTT	TT 1	CTAA	CTGG	3	1297
	GGAA	AAGA	TT	CCCAC	CCAA	T TC	AAAA	CATT	GTG	CCAT	GTC	AAAC	TAAAT	AG 1	CTAI	CTTC	;	1357
	CCAG	ACAC	TG (GTTTG	AAGA	A TG	TTAA	GACT	TGA	CAGT	'GGA	ACTA	CATT	AG 1	CACAC	AGCAC	3	1417
	CAGA	ATGI	AT A	ATTAA	GGTG	T GG	CTTT	'AGGA	GCA	GTGG	GAG	GGTA	.CCGG	CC C	GGTI	AGTA1	C	1477
	CATC	AGAT	CG A	ACTCI	TATA	.C GA	GTAA	TATG	CCT	GCTA	TTT	GAAG	TGTA	AT 1	GAGA	AGGAA	.	1537
25	AATT	TTAG	CG 1	CCTC	ACTG	A CC	TGCC	TGTA	GCC	CCAG	TGA	CAGC	TAGG	AT G	TGCA	TTCT	;	1597
	CAGO	CATO	CAA (GAGAC	TGAG	T CA	AGTT	GTTC	CTT	AAGT	CAG	AACA	.GCAG	AC I	CAGO	TCTGA	L	1657
	CATT	CTGA	TT (CGAAT	'GACA	C TG	TTCA	.GGA.A	TCG	GAAT	CCT	GTCG	ATTA	GA C	TGGA	CAGCT	•	1717
·	TGTG	GCAA	GT (GAATT	TGCC	T GT	AACA	AGCC	AGA	TTTT	TTA	AAAT	TTAT	AT I	GTAA	ATATI	:	1777
	GTGT	GTGT	GT (GTGTG	TGTG	T AT	ATAT	ATAT	ATA	TATG	TAC	AGTT	ATCT	AA G	TTAA	TTTAA		1837



	AGT.	IGIT	IGT	GCCT	TTT	AT T	TTTG	TTTT	T AA	TGCT	TTGA	TAT	TTCA	ATG	TTAG	CCTCAA
	TIT	CTGA	ACA	CCATA	AGGT	AG A	ATGT	AAAG	C TT	GTCT	GATC	GIT	CAAA	GCA '	TGAA	ATGGAT
	ACT:	TATA:	IGG /	AAAT.	ICTG	CT C	AGAT	AGAA'	I GA	CAGT	CCGT	CAA	AACA	GAT	TGTT	TGCAAA
	GGG	GAGG	CAT	CAGT	GTCT:	IG G	CAGG	CTGA:	r tt	CTAG	GTAG	GAA	atgt(GGT .	AGCT	CACG
5	(2)	INF	ORMA'	IION	FOR	SEQ	ID 1	NO:2	•							
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 349 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear															
0	~, * •	(:	ii) l	MOLE	TULE	TYPI	E: p1	rote	in							
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:															
	Met 1	Thr	Ala	Ala	Ser 5	Met	Gly	Pro	Val	Arg 10	Val	Ala	Phe	Val	Val 15	Leu
5	Leu	Ala	Leu	Cys 20	Ser	Arg	Pro	Ala	Val 25	Gly	Gln	Asn	Cys	Ser 30	Gly	Pro
	Cys	Arg	Cys 35	Pro	Asp	Glu	Pro	Ala 40	Pro	Arg	Cys	Pro	Ala 45	Gly	Val	Ser
·	Leu	Val 50	Leu	Asp	Gly	Cys		Cys			Val	Cys 60	Ala	Lys	Gln	Leu
20	Gly 65	Glu	Leu	Cys	Thr	Glu 70	Arg	Asp	Pro	Cys	Asp 75	Pro	His	Lys	Gly	Leu 80
	Phe	Cys	Asp	Phe	Gly 85	Ser	Pro	Ala	Asn	Arg 90	Lys	Ile	Gly	Val	Cys 95	Thr
5	Ala	Lys	Asp	Gly 100	Ala	Pro	Cys	Ile	Phe 105	Gly	Gly	Thr	Val	Tyr 110	Arg	Ser
	Gly	Glu	Ser 115	Phe	Gln	Ser	Ser	Cys 120	Lys	Tyr	Gln	Cys	Thr 125	Cys	Leu	Asp

	Gly	Ala 130	Val	Gly	Cys	Met	Pro 135	Leu	Cys	Ser	Met	Asp 140	Val	Arg	Leu	Pro
	Ser 145	Pro	Aśp	Cys	Pro	Phe 150	Pro	Arg	Arg	Val	Lys 155	Leu	Pro	Gly	Lys	Cys 160
5	Cys	Glu	Glu	Trp	Val 165	Cys	Asp	Glu	Pro	Lys 170	Asp	Gln	Thr	Val	Val 175	Gly
	Pro	Ala	Leu	Ala 180	Ala	Tyr	Arg	Leu	Glu 185	Asp	Thr	Phe	Gly	Pro 190	Asp	Pro
10	Thr	Met	Ile 195	Arg	Ala	Asn	Cys	Leu 200	Val	Gln	Thr	Thr	Glu 205	Trp	Ser	Ala
	Cys	Ser 210	Lys	Thr	Cys	Gly	Met 215	Gly	Ile	Ser	Thr	Arg 220	Val	Thr	Asn	Asp
	Asn 225	Ala	Ser	Cys	Arg	Leu 230	Glu	Lys	Gln	Ser	Arg 235	Leu	Cys	Met	Val	Arg 240
15	Pro	Cys	Glu	Ala	Asp 245	Leu	Glu	Glu	Asn	Ile 250	Lys	Lys	Gly	Lys	Lys 255	Cys
	Ile	Arg	Thr	Pro 260	Lys	Ile	Ser	Lys	Pro 265	Ile	Lys	Phe	Glu	Leu 270	Ser	Gly
20	Суз	Thr	Ser 275	Met	Lys	Thr	Tyr	Arg 280	Ala	Lys	Phe	Cys	Gly 285	Val	Cys	Thr
•	Asp	Gly 290	Arg	Cys	Cys	Thr	Pro 295	His	Arg	Thr	Thr	Thr 300	Leu	Pro	Val	Glu
	Phe 305	Lys	Cys	Pro	Asp	Gly 310	Glu	Val	Met	Lys	Lys 315	Asn	Met	Met	Phe	Ile 320
25	Lys	Thr	Cys	Ala	Cys 325	His	Tyr	Asn	Cys	Pro 330	Gly	Asp	Asn	Asp	Ile 335	Phe
	Glu	Ser	Leu	Tyr 340	Tyr	Arg	Lys	Met	Tyr 345	Gly	Asp	Met	Ala			

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